

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Novel Telomerase

(iii) NUMBER OF SEQUENCES: 225

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997
(C) CLASSIFICATION:

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996
(C) CLASSIFICATION:

(xi) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 015389-002930US

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCAAAAA CCCCTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTAA ATATTAAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120
TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180
TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240
TTATAAAGAT TTAGAAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG	300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360
AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA	420
TAGACAAAAAA CTTCAATGAT TTGGATTTCAC ACTTAAGGGA AATCAATTAG CAAAGACCCA	480
TTTATTAACA GCTCTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCCAAGT	540
TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600
GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAAT AACGTTTTG ATCATTTGAA	660
AGTCAACGAT AAGTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAAACAT	780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACAGA ATATTTTATT GCACTCATT	840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC	900
AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960
GAAGCTAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAAG TCAAAGATT	1020
TAACCTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA	1080
ACAAAAAAATC GAAAACCTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA	1140
GCTGTTTAGC TACACAACTG ATAATAAAAT CGTCACACAA TTTATTAATG AATTTTCTA	1200
CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTC AAAAGAAAGT	1260
TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTACAC AAAAACTTAT TGCTTGAGAA	1320
GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTTATTA	1380
TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT	1440

CGTCGCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCAA 1500
AACCTATTAC TACAGAAAGA ATATTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT 1560
AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT 1620
TGGATTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTCC GTCCAATTAT 1680
GACTTTCAAT AAGAAGATTG TAAATTAGA CCGGAAGACT ACAAAATTAA CTACAAATAC 1740
GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1800
TTTGGATTG GCTGTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTGTTG 1860
CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTGCA ACTATGGATA TCGAAAAGTG 1920
ATATGATAGT GTAAACAGAG AAAAACTATC AACATTCTA AAAACTACTA AATTACTTTC 1980
TTCAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA 2040
TTCGAAAAAC TTAGAAAGA AAGAAATGAA AGATTATTT AGACAGAAAT TCCAGAAGAT 2100
TGCACITGAA GGAGGACAAT ATCCAACCTT ATTCAGTGT CTTGAAAATG AACAAATGA 2160
CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA 2220
TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGAA 2280
GTTTATAAA CAAACAAAAG GAATTCCCTA AGGTCTTGA GTTTCATCAA TTTTGTCATC 2340
ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA 2400
CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC 2460
AACTCAAGAG AATAATGCAG TATTGTTAT TGAGAAACTT ATAAACGTAA GTCGTAAAAA 2520
TGGATTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT 2580
TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
CAAGAAGAAA CCAAAGTCGT TTTAATGAA TAACATTACC CATTATTTA GAAAGACGAT 2820
TACAACCGAA GACTTTGCGA ATAAAACCTC CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
ATACATGCAA TGAGCCAAAG AATACAAGGA CCACCTTAAG AAGAACCTAG CTATGAGCAG 2940
TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
CCTTGTGTGC AATATTAAGG ATACAATTAA TGGAGAGGAG CATTATCCAG ACTTTTCCT 3060
TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATT TCAACAGAGT 3120
TTGCATGATC CTCAAGGCAA AAGAAGCAA GCTAAAAGT GACCAATGTC AATCTCTAAT 3180
TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTGGG AAGTTAATT TCAATTTCG 3240
TCTTATATAC TGGGGTTTG GGGTTTGGG GTTTTGGGG 3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
20 25 30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
85 90 95

Val Glu Leu Leu Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
100 105 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
115 120 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
130 135 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
145 150 155 160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
165 170 175

Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
180 185 190

Asp Lys Lys Gln Lys Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
195 200 205

Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
210 215 220

Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
225 230 235 240

Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
245 250 255

His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
260 265 270

Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
275 280 285

Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
290 295 300

Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
305 310 315 320

Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
325 330 335

Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
340 345 350

Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
355 360 365

Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
370 375 380

Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
385 390 395 400

Lys Asn Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
405 410 415

Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
420 425 430

Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
435 440 445

Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
450 455 460

Tyr Ser Lys Thr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
485 490 495

Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
515 520 525

Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
530 535 540

Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
545 550 555 560

Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
565 570 575

Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
580 585 590

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
595 600 605

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
610 615 620

Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
625 630 635 640

Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
645 650 655

Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly
660 665 670

Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
675 680 685

Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
690 695 700

Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
705 710 715 720

Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
725 730 735

Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
740 745 750

Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
755 760 765

Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
770 775 780

Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
785 790 795 800

Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
805 810 815

Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
820 825 830

Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
835 840 845

Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
850 855 860

Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
865 870 875 880

Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
885 890 895

Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
900 905 910

Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
915 920 925

Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
930 935 940

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
 945 950 955 960
 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
 965 970 975
 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
 980 985 990
 Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005
 Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
 1010 1015 1020
 Ser Leu Ile Gln Tyr Asp Ala
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAAGA	AAAAATTGAG	GTAGTTAGA	60
AATAAAATAT	TATTCCCGCA	CAAATGGAGA	TGGATATTGA	TTTGGATGAT	ATAGAAAATT	120
TACTTCCTAA	TACATTCAAC	AAGTATAGCA	GCTCTTGTAG	TGACAAGAAA	GGATGCAAAA	180
CATTGAAATC	TGGCTCGAAA	TCGCCTTCAT	TGACTATTCC	AAAGTTGCAA	AAACAATTAG	240
AGTTCTACTT	CTCGGATGCA	AATCTTTATA	ACGATTCTTT	CTTGAGAAAA	TTAGTTTTAA	300
AAAGCGGAGA	GCAAAGAGTA	GAAATTGAAA	CATTACTAAT	GTTAAATAA	AATCAGGTAA	360
TGAGGATTAT	TCTATTTTTT	AGATCACTTC	TTAAGGAGCA	TTATGGAGAA	AATTACTTAA	420
TACTAAAAGG	TAAACAGTTT	GGATTATTC	CCTAGCCAAC	AATGATGAGT	ATATTAAATT	480
CATATGAGAA	TGAGTCAAAG	GATCTCGATA	CATCAGACTT	ACCAAAGACA	AACTCGCTAT	540
AAAACGCAAG	AAAAAGTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGCAT	TTACTATTAG	600
TATGGGTTT	ATTACAATTG	TTTTAGGTAT	CGACGGTGAA	CTCCCGAGTC	TTGAGACAAT	660
TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA	AGTTCTGATG	TGTATGCCAT	720
TATTTTGTGA	ATTAATCTCA	AATATCTTAT	CTCAATTAA	TGGATAGCTA	TAGAAACAAA	780
CCAAATAAAC	CATGCAAGTT	TAATGGAATA	TACGTTAAAT	CCTTTGGGAC	AAATGCACAC	840
TGAATTATA	TTGGATTCTT	AAAGCATAGA	TACACAGAAT	GCTTTAGAGA	CTGATTAGC	900
TTACAAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT	AAAAGAAGCA	960

GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTCAAAAT TTGTTGATTCTTCTGTAACC	1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTCTTAAAGATTTC	1080
TTAAAGATTTCAAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG	1140
TTTTCATTT CACAGCTGTT ATTTTCTTT ATCTTAACAA TATTTTTGA TTAGCTGGAA	1200
GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCA	1260
AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTAAAAAA	1320
TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAAA	1380
GAATTGCGTC GATATTGCAA AAGAACATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA	1440
ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTAAAGAAATAAAA	1500
GTAACTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA	1560
TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAAA ATACAAACCT TGGTCAAAAT	1620
ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA	1680
GTACAGAAAGT GAAGAAATAA AAGATTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT	1740
TTGGGGTTTTGGGGTTTTGG GG	1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro	Gln	Asn	Pro	Lys	Thr	Pro	Lys	Pro	Leu	Lys	Lys	Lys	Lys	Lys	Leu	Arg
1																15

Phe	Arg	Asn	Lys	Ile	Leu	Phe	Pro	His	Lys	Trp	Arg	Trp	Ile	Leu	Ile	
20																30

Trp	Met	Ile	Lys	Ile	Tyr	Phe	Leu	Ile	His	Ser	Thr	Ser	Ile	Ala	Ala	
35																45

Leu	Val	Val	Thr	Arg	Lys	Asp	Ala	Lys	His	Cys	Asn	Leu	Ala	Arg	Asn	
50																60

Arg	Leu	His	Cys	Leu	Phe	Gln	Ser	Cys	Lys	Asn	Asn	Ser	Ser	Thr	Ser	
65																80

Arg	Met	Gln	Ile	Phe	Ile	Thr	Ile	Leu	Ser	Cys	Glu	Asn	Phe	Lys	Ala	
85																95

Glu	Ser	Lys	Glu	Lys	Leu	Lys	His	Tyr	Cys	Leu	Asn	Lys	Ile	Arg	Cys	
100																110

Gly	Leu	Phe	Tyr	Phe	Leu	Asp	His	Phe	Leu	Arg	Ser	Ile	Met	Glu	Lys	

115	120	125
Ile Thr Tyr Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys		
130	135	140
Cys Val Tyr Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln		
145	150	155
160		
Thr Tyr Gln Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys Ser		
165	170	175
Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr Tyr		
180	185	190
Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn Cys		
195	200	205
Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys Val		
210	215	220
Cys His Tyr Phe Val Asn Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp		
225	230	235
240		
Ser Tyr Arg Asn Lys Pro Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr		
245	250	255
Val Lys Ser Phe Gly Thr Asn Ala His Cys Ile Tyr Ile Gly Phe Leu		
260	265	270
Lys His Arg Tyr Thr Glu Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln		
275	280	285
Ile Thr Cys Phe Asp Tyr Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu		
290	295	300
Ala Gly Glu Met Lys Arg Arg Leu Lys Lys Glu Ile Ser Lys Phe Val		
305	310	315
320		
Asp Ser Ser Val Thr Gly Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys		
325	330	335
Glu Glu Glu Leu Ser Gln Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro		
340	345	350
Gly Lys Arg Asp Thr Phe Ile Lys Ile His Ile Leu Phe Phe Ile Ser		
355	360	365
Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe Asp Leu Glu Val		
370	375	380
Lys Ser Ile Lys Glu Lys Arg Thr Glu Val Thr Leu Ile His Ile His		
385	390	395
400		
Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys Gly Asn Ser Ser His Pro		
405	410	415
Phe Lys Cys Tyr Glu Asp Ile Phe Arg Val Lys Lys Trp Ser Arg Asn		
420	425	430
Leu Asn Gln Lys Glu Leu Arg Arg Tyr Cys Lys Arg Ile Glu Leu Ile		
435	440	445

Phe Arg Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Arg Gly Asn Cys
 450 455 460
 Thr Glu Asp His Arg Asn Lys Val Thr Phe Ile Asn Arg Ile Asn Ile
 465 470 475 480
 Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys Lys Leu Asn Ser
 485 490 495
 Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu
 500 505 510
 Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln Ile Lys Cys Val Gln Lys
 515 520 525
 Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu Lys Arg Gly
 530 535 540
 Val Leu Gly Phe Trp Gly Phe Gly
 545 550

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys
 1 5 10 15
 Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr
 20 25 30
 Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser Tyr Ile Gln Gln Val Gln
 35 40 45
 Leu Leu Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala
 50 55 60
 Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu
 65 70 75 80
 Gly Cys Lys Ser Leu Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys
 85 90 95
 Arg Arg Ala Lys Ser Arg Asn Cys Asn Ile Thr Asn Val Ile Lys Ser
 100 105 110
 Gly Asn Glu Asp Tyr Ser Ile Phe Ile Thr Ser Gly Ala Leu Trp Arg
 115 120 125
 Lys Leu Leu Asn Thr Lys Arg Thr Val Trp Ile Ile Ser Leu Ala Asn
 130 135 140
 Asn Asp Glu Tyr Ile Lys Phe Ile Cys Glu Cys Val Lys Gly Ser Arg
 145 150 155 160

Tyr Ile Arg Leu Thr Lys Asp Lys Leu Ala Ile Lys Arg Lys Lys Lys
165 170 175

Phe Asp Asn Arg Thr Ala Glu Glu Leu Ile Ala Phe Thr Ile Arg Met
180 185 190

Gly Phe Ile Thr Ile Val Leu Gly Ile Asp Gly Glu Leu Pro Ser Leu
195 200 205

Glu Thr Ile Glu Lys Ala Val Tyr Asn Cys Arg Asn Arg Ser Ser Glu
210 215 220

Ser Ser Asp Val Tyr Ala Ile Ile Leu Cys Ile Asn Leu Lys Tyr Leu
225 230 235 240

Ile Ser Ile Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser
245 250 255

Leu Met Glu Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe
260 265 270

Ile Leu Asp Ser Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu
275 280 285

Ala Tyr Asn Arg Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr
290 295 300

Leu Lys Lys Gln Ala Lys Cys Lys Glu Asp Arg Lys Arg Phe Gln Asn
305 310 315 320

Leu Leu Ile Leu Leu Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys
325 330 335

Lys Lys Lys Ser Tyr His Asn Pro Asp Ser Arg Phe Gln Lys Phe Gln
340 345 350

Val Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe
355 360 365

His Ser Cys Tyr Phe Leu Leu Ser Gln Tyr Phe Leu Ile Ser Trp Lys
370 375 380

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg Leu Ser Leu Phe Thr
385 390 395 400

Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu Thr Ala
405 410 415

Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu Glu Ser
420 425 430

Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp Ile Ala
435 440 445

Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln Ser Cys
450 455 460

Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile Lys Glu
465 470 475 480

Ile Lys Leu Leu Leu Ile Arg Glu Thr Lys Leu Leu Ile Arg Ser Ala
485 490 495

Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg Gln Lys Ile
 500 505 510
 Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser Gln Lys
 515 520 525
 Lys Lys Gly Asn Lys Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu
 530 535 540
 Phe Phe Ser Ile Ile Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val
 545 550 555 560
 Leu Gly

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
 1 5 10 15
 Val Val Lys Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu
 20 25 30
 Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser
 35 40 45
 Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys
 50 55 60
 Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr
 65 70 75 80
 Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val
 85 90 95
 Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe
 100 105 110
 Lys Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys
 115 120 125
 Glu His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly
 130 135 140
 Leu Phe Pro Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu
 145 150 155 160
 Ser Lys Asp Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu Asn
 165 170 175
 Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His Leu
 180 185 190

Leu Phe Val Trp Val Leu Leu Gln Leu Phe Val Ser Thr Val Asn Ser
 195 200 205
 Arg Val Leu Arg Gln Leu Lys Lys Leu Phe Thr Thr Glu Gly Ile Ala
 210 215 220
 Val Leu Lys Val Leu Met Cys Met Pro Leu Phe Cys Glu Leu Ile Ser
 225 230 235 240
 Asn Ile Leu Ser Gln Phe Asn Gly Leu Lys Gln Thr Lys Thr Met Gln
 245 250 255
 Val Trp Asn Ile Arg Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr
 260 265 270
 Trp Ile Leu Lys Ala Ile His Arg Met Leu Arg Leu Ile Leu Thr Thr
 275 280 285
 Asp Tyr Leu Phe Cys Leu Leu Leu Ile Ser Tyr Ile Phe Lys Arg
 290 295 300
 Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe Lys Ile Cys
 305 310 315 320
 Cys Phe Phe Cys Asn Arg Asn Gln Gln Glu Tyr Gln Arg Lys Arg Arg
 325 330 335
 Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe Lys Asn Ser Arg Glu
 340 345 350
 Arg Tyr Ile His Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val
 355 360 365
 Ile Phe Phe Tyr Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys
 370 375 380
 Tyr Gln Ile Arg Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His
 385 390 395 400
 Ser Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser
 405 410 415
 Ser Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe Ser Gln Glu Met
 420 425 430
 Glu Pro Lys Ser Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg
 435 440 445
 Thr Leu Asn Leu Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys
 450 455 460
 Arg Leu Thr Arg Gln Leu His Arg Arg Ser Leu Lys Lys Ser Asn Phe
 465 470 475 480
 Tyr Leu Glu Asn Lys Leu Asn Tyr Tyr Arg Asp Gln Arg Ser Ser Ile
 485 490 495
 Asp Glu Ile Lys Ala Glu Leu Lys Leu Asp Asn Lys Lys Tyr Lys Pro
 500 505 510
 Trp Ser Lys Tyr Cys Gly Arg Lys Arg Arg Pro Val Ser Lys Arg Lys
 515 520 525

Asn Lys Ala Ile Asn Lys Met Ser Thr Glu Val Lys Lys Lys Ile Tyr
530 535 540

Phe Phe Gln Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu
1 5 10 15

Trp Trp Glu Leu Glu Leu Met Gln Glu Asn Gln Asn Asp Ile Gln
20 25 30

Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr
35 40 45

Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu
50 55 60

Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp
65 70 75 80

Pro Glu Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr
85 90 95

Ile Arg Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys
100 105 110

Asn Thr Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu
115 120 125

Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile
130 135 140

Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser
145 150 155 160

Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys
165 170 175

Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr
180 185 190

Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val
195 200 205

Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn
210 215 220

Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys
225 230 235 240

Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
 245 250 255
 Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
 260 265 270
 Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
 275 280 285
 Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
 290 295 300
 Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
 305 310 315 320
 Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
 325 330 335
 Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
 340 345 350
 Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
 355 360 365
 Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
 370 375 380
 Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
 385 390 395 400
 Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
 405 410 415
 Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
 420 425 430
 Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
 435 440 445
 Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
 450 455 460
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
 465 470 475 480
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
 485 490 495
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
 500 505 510
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
 515 520 525
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
 530 535 540
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
 545 550 555 560
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
 565 570 575

Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460

Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
 850 855 860
 Tyr Asp Tyr Asn Ser Asp Arg Trp
 865 870

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn
 1 5 10 15
 Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys
 20 25 30
 Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln
 35 40 45
 Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu
 50 55 60
 Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr
 65 70 75 80
 Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
 1 5 10 15
 Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
 20 25 30

Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys		
														40	45		
35																	
Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln		
														50	55	60	
65																	
Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	Ile	Asn	Cys	Ile	Leu	Asp	Gln	His		
															70	75	80
85																	
Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys		
															90		95
100																	
Ala	Phe	Ile	Leu														
100																	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Glu	Met	Asp	Ile	Asp	Leu	Asp	Asp	Ile	Glu	Asn	Leu	Leu	Pro	Asn			
1																15		
5																		
Thr	Phe	Asn	Lys	Tyr	Ser	Ser	Ser	Cys	Ser	Asp	Lys	Lys	Gly	Cys	Lys			
															20	25	30	
20																		
Thr	Leu	Lys	Ser	Gly	Ser	Lys	Ser	Pro	Ser	Leu	Thr	Ile	Pro	Lys	Leu			
															35	40	45	
35																		
Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn	Asp			
															50	55	60	
50																		
Ser	Phe	Leu	Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val	Glu			
															65	70	75	80
65																		
Ile	Glu	Thr	Leu	Leu														
85																		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile	Glu	Leu	Ala	Ile	Lys	Ile	Ala	Val	Asn	Lys	Asn	Leu	Asp	Glu	Ile		
1																15	
5																	
20																	
Lys	Gly	His	Thr	Ala	Ile	Phe	Ser	Asp	Val	Ser	Gly	Ser	Met	Ser	Thr		
															20	25	30
20																	

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
35 40 45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
50 55 60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Lys Cys Tyr
65 70 75 80

Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys
85 90 95

Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1 5 10 15

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20 25 30

Leu Leu Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
35 40 45

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser
50 55 60

Ser Leu Gly Phe Leu
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15

Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30

Ile Asn Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser
35 40 45

Leu Ser Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln
50 55 60

Leu His Asn Asp Arg
65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
20 25 30

Ser Asp His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro
35 40 45

Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg
50 55 60

Leu Ala Gly Leu Ala
65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
20 25 30

Ile Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys
35 40 45

Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro
50 55 60

Phe Arg Lys Gln Asn
65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15

Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
20 25 30

Lys Asn Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
35 40 45

Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe
50 55 60

Tyr Ser Glu Phe Lys
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1 5 10 15

Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
20 25 30

Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Gln Asp Tyr Cys Asp
35 40 45

Trp Ile Gly Ile Ser Ile
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
1 5 10 15

Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
20 25 30

Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr Lys Cys Leu Tyr Lys
35 40 45

Tyr Leu Gly Phe Gln Gln
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15

Asn Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly
20 25 30

Leu Thr Ile Asn Glu Glu Lys Thr Leu Ile Glu Thr Pro Ala Arg Phe
35 40 45

Leu Gly Tyr Asn Ile
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
1 5 10 15

Gly His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp
20 25 30

Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu
35 40 45

Trp Met Gly Tyr Glu Leu
50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15

Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
20 25 30

Asn Ala Lys Ala Asn Arg Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe
35 40 45

Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
1 5 10 15

Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
20 25 30

Glu Ile Glu Thr Leu Leu Met
35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Cys His Gln Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg Asp
1 5 10 15

Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro Leu
20 25 30

Glu Ile Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1 5 10 15

Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
20 25 30

Leu Glu Thr Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg
1 5 10 15

Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val
20 25 30

Pro Leu Ser Val Leu Val Thr
35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr
1 5 10 15

Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro
20 25 30

Ile Ser Thr Ile Ala Thr
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGTACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AACCTAACCA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCAGGAATTCTAATACGACTCACTATAGGGAAAGAAACTCTGATGAGGCCGAAAGGCCGAA 60

ACTCCACGAAAGTGGAGTAA GTTTCTCGATAATTGATCTGTAG 103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCTCTTCAAAAGATGAGAGGACAGCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAACCCCAAAACCCCCAACAGGGGTTTGGGGGTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCCCAAACCCCCACAGGGGTTTGGGGGTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCAAAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCAAAAA CCCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCAAAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCCAAAACC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "RNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "RNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAAYCCWGar AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATT	TAATCAACAA	GATTGATAAA	AAGCAGTAAA	TAAAACCCAA	60
TAGATTTAAT	TTAGAAAGTA	TCAATTGAAA	AATGGAAATT	GAAAACAAC	120
GCCAAAAGCC	GAAAAATTGT	GGTGGGAAC	TGAATTAGAG	ATGCAAGAAA	180
TATATAAGTT	AGGGTTAAC	GA TTGACGATCC	TAAGCAATAT	CTCGTGAACG	240
ATGTTTGITG	TAGGAAGGTA	GTTACTACTA	AGATAAAAGAT	GAAAGAAGAT	300
TAAAGCACTT	CTTGAGGTGG	CTGAGTCTGA	TCCTGAGTTC	ATCTGCTAGT	360
CATCCGTAAT	GAAC	TTTACA	TCAGAACTAC	CACTAACTAC	420
CCACAAGAAT	ACTCAACC	CAT	TCATCGAAA	GTACTTCAAC	480
TGACTTACTG	GAAGTCTGTG	AATTTGCATA	GGTTCTCTAT	ATTTTGATG	540
CAAAAATTG	TATCTTGATA	GGATACTTTC	ATAAGATATT	CGTAAGGAAC	600
TAAGTGT	TTA CAAAGATGCG	TCAGAAGCAA	GTTTCTGAA	TTCAACGAAT	660
TAAGTATTGC	ACTGAATCCT	AACGTAAGAA	AACAATGTT	CGTTACCTCT	720
CAAGTAAAAG	TGGGATTAAA	CTAAGAAGAA	GAGAAAAGAG	AATCTCTAA	780
GGCAATAAAG	GAATCTGAAG	ATAAGTCAA	GAGAGAAACT	GGAGACATAA	840
AGATGCAATC	AAGGCTTAA	AACCAGCAGT	TATGAAGAAA	ATAGCCAAGA	900
CATGAAGAAA	CACATGAAGG	CACCTAAAT	TCCTAACTCT	ACCTTGGAA	960
GACCTTCAAG	GATCTCATTA	AGTTCTGCCA	TATTTCTGAG	CCTAAAGAAA	1020
GATCCTTGGT	AAAAAATACC	CTAAGACCGA	AGAGGAATAC	AAAGCAGCCT	1080
TGCATCTGCA	CCCTTCAATC	CTGAATTGGC	TGGAAAGCGT	ATGAAGATTG	1140
AACATGGGAA	AATGAAC	TC GTGCAAAG	CAACACTGCT	GAGGTTGGG	1200
TTCAAGCAAT	TAAC	CTCCC	CAT ATATGGCC	GTACGTAAC	1260
CGGTGTTCA	GATACTACAC	ACTCTATTGT	GATCAACAA	ATTTGTGAGC	1320
TGAGAACTCC	AAGATGTTCC	CTCTTCAATT	CTTTAGTGCC	ATTGAAGCTG	1380
AGTTACTAAG	GGATTCAAGG	CCAAGAAGAG	AGAAAATATG	AATCTAAAG	1440
AGCAGTAAAG	GAAGTTGTTG	AAAAAACCGA	TGAAGAGAAG	AAAGATATGG	1500

AACCGAAGAA GGAGAATTG TTAAAGTC	1560
CATTGAAC	1620
TGCAATCTTC TCTGATGTT	1680
GTATGGTCC GTTCGTACTT	1740
ACGTTGTGAA AAGTCCTCAT	1800
TTACTTAGAA GTTGATCTCC	1860
AGAGAAAGGA AAACTTGGTG	1920
AAAGAATAAA ACTCACGTAG	1980
ATATTCA GAT ATCAATGTTA	2040
TGAAGTAAAT CCTAACATTA	2100
TAATCTAGGT GATGAGTTCA	2160
AATCTTAAAG TTCATTCAG CCAAGCAAGG	2220
CTTTGCCCTT CAAAAAATAG GACAAAAGTG	2280
CTCACCCCCAC TTTTTGTTT TATTGCATAG	2340
ATTTAAGTTA CTTACATAGT TTATGTATCG	2400
AAAGAACAAA AAAGATTAAA A	2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg
1					5							10		15	
Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala
					20				25			30			
Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg
					35				40			45			
Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu
					50				55			60			
Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg
					65				70			75		80	
Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr
					85				90			95			

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn
 100 105 110
 Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp
 115 120 125
 Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp
 130 135 140
 Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg
 145 150 155 160
 Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr
 165 170 175
 Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn
 180 185 190
 Lys Gln Lys Trp Asp Gln Thr Lys Lys Arg Lys Glu Asn Leu Leu
 195 200 205
 Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu
 210 215 220
 Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro
 225 230 235 240
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His
 245 250 255
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu
 260 265 270
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu
 275 280 285
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu
 290 295 300
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu
 305 310 315 320
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn
 325 330 335
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile
 340 345 350
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn
 355 360 365
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn
 370 375 380
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu
 385 390 395 400

Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540
 Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly
 545 550 555 560
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys
 565 570 575
 Leu Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr
 580 585 590
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met
 595 600 605
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val
 610 615 620
 Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile
 625 630 635 640
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp
 645 650 655
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser
 660 665 670
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu
 675 680 685
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly
 690 695

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2829 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAAA GCAAAC TACA AAGAAAATGT CAAGGCGTAA	60
CTAAAAAAAG CCATAGGCTC CTATAGGCAA TGAAACAAAT CTTGATTTG TATTACAAAA	120
TCTAGAAGTT TACAAAAGCC AGATTGAGCA TTATAAGACC TAGTAGTAAT AGATCAAAGA	180
GGAGGATCTC AAGCTTTAA AGTCAAAAA TTAAGATTAG GATGGAAACT CTGGCAACGA	240
TGATGATGAT GAAGAAAACA ACTCAAATAA ATAATAAGAA TTATTAAGGA GAGTCATTAA	300
GATTAAGTAG CAAGTTAAT TGATAAAAAA AGTTGGTTCT AAGGTAGAGA AAGATTTGAA	360
TTTGAACGAA GATGAAAACA AAAAGAATGG ACTTTCTGAA TAGCAAGTGA AAGAAGAGTA	420
ATTAAGAACG ATTACTGAAG AATAGGTTAA GTATTAAAAT TTAGTATTAA ACATGGACTA	480
CCAGTTAGAT TAAATGAGA GTGGTGGCCA TAGAAGACAC AGAAGAGAAA CAGATTATGA	540
TACTGAAAAA TGGTTGAAA TATCTCATGA CCAAAAAAT TATGTATCAA TTTACGCCAA	600
CTAAAAGACA TCATATTGTT GGTGGCTTAA AGATTATTTT AATAAAACA ATTATGATCA	660
TCTTAATGTA AGCATTAACA GACTAGAAAC TGAAGCCGAA TTCTATGCCT TTGATGATT	720
TTCACAAACA ATCAAACCTA CTAATAATT CTAATTAGACT GTTAACATAG ACGTTAATT	780
TGATAATAAT CTCTGTATAC TCGCATTGCT TAGATTTTTA TTATCACTAG AAAGATTCAA	840
TATTTTGAA ATAAGATCTT CTTATACAAG AAATTAATAT AATTTGAGA AAATTGGTGA	900
GCTACTTGAA ACTATCTCG CAGTTGTCTT TTCTCATCGC CACTTACAAG GCATTCAATT	960
ACAAGTTCCCT TGCGAAGCGT TCTAATATTT AGTTAACTCC TCATCATAAA TTAGCGTTAA	1020
AGATAGCTAA TTATAGGTAT ACTCTTCCTC TACAGACTTA AAATTAGTTG ACACTAACAA	1080
AGTCCAAGAT TATTTTAAGT TCTTATAAGA ATTCCCTCGT TTGACTCATG TAAGCTAGTA	1140
GGCTATCCC GTTAGTGCTA CTAACGCTGT AGAGAACCTC AATGTTTAC TTAAAAAGGT	1200
CAAGCATGCT AATCTTAATT TAGTTCTAT CCCTACCTAA TTCAATTGTT ATTTCTACTT	1260
TGTTAATTAA TAACATTGAA AATTAGAGTT TGGATTAGAA CCAAATATTT TGACAAAACA	1320
AAAGCTTGAA AATCTACTTT TGAGTATAAA ATAATCAAAA AATCTAAAT TTTTAAGATT	1380
AAACTTTAC ACCTACGTTG CTAAAGAAC CTCCAGAAAA CAGATATTAA ACAAGCTAC	1440
AACAATCAAA AATCTAAAAA ACAATAAAA TCAAGAAGAA ACTCCTGAAA CTAAAGATGA	1500
AACTCCAAGC GAAAGCACAA GTGGTATGAA ATTTTTGAT CATCTTCTG AATTAACCGA	1560
GCTTGAAGAT TTCAGCGTTA ACTTGTAAGC TACCCAAGAA ATTTATGATA GCTTGCACAA	1620

ACTTTTGATT AGATCAACAA ATTTAAAGAA GTTCAAATTA AGTTACAAAT ATGAAATGGA	1680
AAAGAGTAAA ATGGATACAT TCATAGATCT TAAGAATATT TATGAAACCT TAAACAATCT	1740
TAAAAGATGC TCTGTTAATA TATCAAATCC TCATGGAAAC ATTTCTTATG AACTGACAAA	1800
TAAAGATTCT ACTTTTATA AATTTAAGCT GACCTTAAAC TAAGAATTAT AACACGCTAA	1860
GTATACTTTT AAGTAGAACG AATTTTAATT TAATAACGTT AAAAGTCAA AAATTGAATC	1920
TTCCTCATTA GAAAGCTTAG AAGATATTGA TAGTCTTGC AAATCTATTG CTTCTTGTAA	1980
AAATTTACAA AATGTTAATA TTATGCCAG TTTGCTCTAT CCCAACAAATA TTTAGAAAAA	2040
TCCTTCAAT AAGCCAATC TTCTATTTT CAAGCAATT GAATAATTGA AAAATTTGGA	2100
AAATGTATCT ATCAACTGTA TTCTTGATCA GCATATACTT AATTCTATT CAGAATTCTT	2160
AGAAAAGAAT AAAAAAATAA AAGCATTCA TTTGAAAAGA TATTATTTAT TACAATATTA	2220
TCTTGATTAT ACTAAATTAT TTAAAACACT TCAATAGTTA CCTGAATTAA ATTAAGTTA	2280
CATTAATTAG CAATTAGAAG AATTGACTGT GAGTGAAGTA CATAAGTAAG TATGGAAAAA	2340
CCACAAGCAA AAAGCTTCT ATGAACCATT ATGTGAGTTT ATCAAAGAAT CATCCTAAAC	2400
CCTTAGCTA ATAGATTTG ACCAAAACAC TGTAAGTGAT GACTCTATTA AAAAGATTT	2460
AGAATCTATA TCTGAGTCTA AGTATCATCA TTATTTGAGA TTGAACCTA GTTAATCTAG	2520
CAGTTTAATT AAATCTGAAA ACGAAGAAAT TTAAGAACTT CTCAAAGCTT GCGACGAAA	2580
AGGTGTTTA GTAAAAGCAT ACTATAAATT CCCTCTATGT TTACCAACTG GTACTTATT	2640
CGATTACAAT TCAGATAGAT GGTGATTAAT TAAATATTAG TTTAAATAAA TATTAAATAT	2700
TGAATATTTTC TTTGCTTATT ATTTGAATAA TACATACAAT AGTCATTTT AGTGTGTTGA	2760
ATATATTTTA GTTATTTAAT TCATTATTTT AAGTAAATAA TTATTTTCA ATCATTNTTT	2820
AAAAAATCG	2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ser	Arg	Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	Pro	Ile	Gly	Asn	Glu
1						5						10			15

Thr	Asn	Leu	Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	Val	Tyr	Lys	Ser	Gln
					20				25				30		

Ile	Glu	His	Tyr	Lys	Thr	Gln	Gln	Gln	Ile	Lys	Glu	Glu	Asp	Leu
					35			40				45		

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60

Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95

Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110

Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140

Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160

Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175

Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190

Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205

Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220

Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240

Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255

Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270

Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285

Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300

Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320

Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335

Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350

Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365

Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380

Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
385 390 395 400

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
405 410 415

Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
420 425 430

Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
435 440 445

Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
450 455 460

Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
465 470 475 480

Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
485 490 495

Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
500 505 510

Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
515 520 525

Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
530 535 540

Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
545 550 555 560

Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
565 570 575

Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
580 585 590

Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
595 600 605

Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
610 615 620

Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
625 630 635 640

Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
645 650 655

Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
660 665 670

Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
675 680 685

Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
690 695 700

Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
 850 855 860
 Tyr Asp Tyr Asn Ser Asp Arg Trp
 865 870

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 884 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
 1 5 10 15
 Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
 20 25 30
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
 115 120 125
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
 130 135 140
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
 145 150 155 160
 Trp Val Gln Arg Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
 165 170 175
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro
 305 310 315 320
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
 325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
450 455 460

Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
465 470 475 480

Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
485 490 495

Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
500 505 510

Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
515 520 525

Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
530 535 540

Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
545 550 555 560

Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
565 570 575

Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
580 585 590

Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
595 600 605

Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
610 615 620

Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
625 630 635 640

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
645 650 655

Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
660 665 670

Leu Ile Ile Ser Thr Asp Gln Gln Val Ile Asn Ile Lys Lys Leu
675 680 685

Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
690 695 700

Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
705 710 715 720

Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
725 730 735

Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
740 745 750

Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
755 760 765

Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
785 790 795 800

Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
805 810 815

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
820 825 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
835 840 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
850 855 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
1 5 10 15

Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
20 25 30

Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
1 5 10 15

Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
20 25 30

Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "RNA"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..25
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "The residues located at these positions are
2-O-methylribonucleoti..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAGACCTGTT AGGUUUUUGGG GUUUUG

26

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTGGG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGCACGGCT GATGAGTGTG TACGTCGTCG AGCTGCTCAG GTCTTTCTTT	60
TATGTCACGG AGACCACGTT TCAAAAGAAC AGGCTCTTT TCTACCGGAA GAGTGTCTGG	120
AGCAAGTTGC AAAGCATTGG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG	180
TCGGAAGCAG AGGTCAAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC	240
CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA	300
GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCAGTG	360
TTCAGCGTGC TCAACTACGA GCGGGCGCG	389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys			
1	5	10	15

Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe		
20	25	30

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
 35 40 45

Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
 50 55 60

Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
 65 70 75 80

Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
 85 90 95

Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
 100 105 110

Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
 115 120 125

Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 130 135 140

Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
 145 150 155 160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175

Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190

Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205

Phe Arg Ile Val Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220

Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
 1 5 10 15

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30

Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45

Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60

Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80

Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95

Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110

Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125

Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140

Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys
 145 150 155 160

Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln
 165 170 175

Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
 180 185 190

Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
 195 200 205

Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
 210 215 220

Arg Ser Gln Tyr Phe Phe Asn Thr Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplates aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2631
 - (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTAAA ATGTGGTCAC TTCAATGCC TCGATGAAAT	120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAAATAG	300
TCTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGGCCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATAKGATT CGTTGATTAA TTGATCAATT ATACAGTAAT	420
TCAATTAAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GCCGCCAAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCCTTTC	600
TTTTTTCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTTCCCA CAAATTGGT TAAAATTCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATT	780
GAATAGTATT TGCCCACCATT TGGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAATTATC AAGAATCTAA ATCTTTTATT	960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTG TTGAAAAGT TAAGATTAAA	1020
GGATTTCCGG TGGTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCTT	1080
GAATCAATTG GCGATTGTT TCATTTCTG GCTATTAGA CAACTAATTC CCAAAATTAT	1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA	1200
TGATACTTGG AATAAACTTA TCACCCCTT TATCGTAGAA TATTTAAGA CGTACTTAGT	1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTCA ATCATAGCAA	1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTCAGG ATTATTGCCA TCCCAGTCAG	1380
AGGGGCAGAC GAAGAAGAAT TCACAATTAA TAAGGAGAAT CACAAAATG CTATCCAGCC	1440
CACTCAAAAA ATTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTA CTAAAATATA	1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTAAAG CAGAGACTTT TAAAGAAATT	1560
TAATAATGTC TTACCAAGAC TTTATTCTAT GAAATTGAT GTCAAATCTT GCTATGATTC	1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCC CTAAAAAATG AAAATGGGTT	1680
TTTCGTTAGA TCTCAATATT TCTTCATAAC CAATACAGGT GTATTGAAGT TATTTAATGT	1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT	1800

TCATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTT	1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC	1920
TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC	1980
CAGTCCTAGC CAGGACACAT TAATTTAAA ACTGGCTGAC GATTCCTTA TAATATCAAC	2040
AGACCAAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GGCGGATTTC AAAAATATAA	2100
TGCGAAAGCC AATAGAGACA AAATTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT	2160
TATTCAATT TGTGCAATGC ACATATTGT TAAAGAATTG GAAGTTGGA AACATTCAAG	2220
CACAATGAAT AATTCCATA TCCGTTCGAA ATCTAGTAA GGGATATTTC GAAGTTAAT	2280
AGCGCTGTT AACACTAGAA TCTCTTATAA ACAATTGAC ACAATTAA ATTCAACAAA	2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC	2400
TTTTAAGGAT CTATCAATT AATGTTACGCA AAATATGCAA TTTCATTCGT TCTTACAACG	2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA	2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTCAA ACACATCAA	2580
ATTTAAAGAT AATATCATT CTTTGAGAAA GGAAATTCAA CACTTGCAAG C	2631

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu			
1	5	10	15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu			
20	25	30	

Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile			
35	40	45	

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu			
50	55	60	

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu			
65	70	75	80

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 85 90 95
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 100 105 110
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 115 120 125
 Ala

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543,
1595..1857, 1894..2286, 2326..2396, 2436..2705,
2746..2862, 2914..3083, 3125..3309, 3356..3504,
3546..3759, 3797..4046, 4086..4252, 4296..4392,
4435..4597)
- (D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe
telomerase catalytic subunit (TRT)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAA GT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTAC TTTATTAATT TACTTTCAA ATATATTCG	240
GGTCGCTTA CTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGT	300
TCTACCCCGT CATTGGATAT AGCTCTGGAA GTAGCTCACA GAAATCCTTA CAAATCTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATT CTTAACATGGAA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTGAT	540
GCTTGCACAC GTCTAGCATG ATTGAGATAT TCAAAAATT CTATCCACTA CAACTCCTT	600
AACGCGGTTT TATTTCTATT CTCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTT ACTCCTGGAA TCGTACCTTT TTCACTATT CCCCTAATGA	720
ATAATCTAAA TTAGTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780

TGTAATGTTA TTAGTTAAA GATACTTGC AAAACATTAA TAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAAT ATTAATCAAT ATTTGCGGTC ACTATTATT TAAAACGTTA	900
TGATCAGTAG GACACTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	1006
1 5 10 15	
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	1054
20 25 30	
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	1102
35 40 45	
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	1150
50 55 60	
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro	1198
65 70 75 80	
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTGTTG ATTTTTTTCT Lys Cys Ser Gln Ser Glu	1246
85	
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met	1299
90 95	
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Asn Leu Leu Met Lys Gly Phe	1347
100 105 110	
TCC ATG GTAAAGGTATT CTAATTGTGA AATATTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val	1454
115 120	
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile	1502
125 130 135	
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Glu Ile	1543
140 145 150	
GTAAATACCG GTAAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu	1646
155 160 165 170	

GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAACTAATA CTGTTATCCT TCATAACTAA Tyr Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAAG AC 2327 Glu Ile Ile Leu Lys 370	Asp
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys	2426

390

395

AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser 400	405	2474
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe 410	415	420
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu 425	430	435
CAA TCT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr 445	450	455
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile 460	465	470
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTAAA Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu 475	480	485
GTATTTTTG CAAAAAGCTA ATATTTCACT AAC AAT GTT AGG ATG GAT ACT CAG Asn Asn Val Arg Met Asp Thr Gln 490		2769
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn 495	500	505
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys 510	515	520
GTATTAATT TGGTCATCA ATGTACTTTA CTTCTAACCT ATTATTAGCA G ATG GGT Met Gly 525		2919
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val 530	535	540
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA Ala Ser Ile Leu Lys His Leu Ile Asn Glu Ser Ser Gly Ile Pro 545	550	555
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu 560	565	570
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT Leu Lys His Arg Met Phe Gly 575	580	3113
TAATTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser 585	590	3161

TST TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTCATTG GAATTTTTA ACAAAATTCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATAACCAAT TGTTGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCTA AGTTCTAACCG TTGAAG GA Leu Ser Leu Arg Gly 760	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu	3942

	800	805	810	
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser	815	820	825	3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys	830	835	840	4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg			Ser	4089
	845			
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser	850	855	860	4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys	865	870	875	4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro	885	890	895	4233
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr	900			4282
TAATTTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys	905		910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser	915	920	925	4378
GCA GAA GTC AAA TG GTACGTGTG GTCTCGAGAC TTTCAGCAATA TTGACACATC Ala Glu Val Lys Trp	935			4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys	940	945	950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr	955	960	965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu	970	975	980	4576
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC His Arg Arg Ile Ala Asp	985			4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC				4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTGGA TTGACTTGTC				4744

TTTATCCTTA TACTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCA	4804
TTAACGGGA GTGGTTAAC ATTAAAAGTA ATACATGAGG CTAATTCCT TTCATTTAGA	4864
ATAAGGAAAG TGTTTTCTA TAATGAATAA TGCCCGCACT AATGAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTGG	5044
TGACCGAATT TTGGTAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAAACT AAGGATAGTT TGAATACTAA TAGCTCATT AATGTCTTAT ATAAGGTTTT	5164
GTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTAAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTTC TTGGTTCCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAAATC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTG CAAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524
GTAAAGTGAC CAAAGGTACC	5544

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 988 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Thr	Glu	His	His	Thr	Pro	Lys	Ser	Arg	Ile	Leu	Arg	Phe	Leu	Glu
1					5					10				15	
Asn	Gln	Tyr	Val	Tyr	Leu	Cys	Thr	Leu	Asn	Asp	Tyr	Val	Gln	Leu	Val
					20				25				30		
Leu	Arg	Gly	Ser	Pro	Ala	Ser	Ser	Tyr	Ser	Asn	Ile	Cys	Glu	Arg	Leu
					35				40				45		
Arg	Ser	Asp	Val	Gln	Thr	Ser	Phe	Ser	Ile	Phe	Leu	His	Ser	Thr	Val
					50				55				60		
Val	Gly	Phe	Asp	Ser	Lys	Pro	Asp	Glu	Gly	Val	Gln	Phe	Ser	Ser	Pro
					65				70				75		80
Lys	Cys	Ser	Gln	Ser	Glu	Leu	Ile	Ala	Asn	Val	Val	Lys	Gln	Met	Phe
					85				90				95		
Asp	Glu	Ser	Phe	Glu	Arg	Arg	Asn	Leu	Leu	Met	Lys	Gly	Phe	Ser	
					100				105				110		
Met	Asn	His	Glu	Asp	Phe	Arg	Ala	Met	His	Val	Asn	Gly	Val	Gln	Asn

115	120	125
Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile Ser Ile Leu Glu Ser		
130	135	140
Lys Asn Trp Gln Leu Leu Leu Glu Ile Ile Gly Ser Asp Ala Met His		
145	150	155
Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu Ala Leu Pro Asn Asp Asn		
165	170	175
Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe Lys Asn Asn Val Phe Glu		
180	185	190
Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr		
195	200	205
Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile		
210	215	220
Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln		
225	230	235
Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His		
245	250	255
Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala		
260	265	270
Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser		
275	280	285
Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln		
290	295	300
Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His		
305	310	315
Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr		
325	330	335
Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val		
340	345	350
Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile		
355	360	365
Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser		
370	375	380
Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu		
385	390	395
Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp		
405	410	415
Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr		
420	425	430
Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu		
435	440	445

Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
450 455 460

Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
465 470 475 480

Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
485 490 495

Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
500 505 510

Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
515 520 525

Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
530 535 540

Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
545 550 555 560

Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
565 570 575

His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
580 585 590

Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
595 600 605

Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
610 615 620

His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
625 630 635 640

Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
645 650 655

Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
660 665 670

Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
675 680 685

His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
690 695 700

Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
705 710 715 720

Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Gly Ser Val
725 730 735

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
740 745 750

Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
755 760 765

Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
770 775 780

Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_bases= OTHER
 /note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRIC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACCT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATT	180
CAGAAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAAC TA TTGTCAAAGT AAGAATTAG TTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTATC AAAAAATT A GCTTGAAGAG GAGAATTGAG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTA GAAATACCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTA GGAATTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp			
1	5	10	15

Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser		
20	25	30

Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu		
35	40	45

Glu Glu Glu Asn Leu Glu Lys Val Glu Lys Leu Ile Pro Glu Asp		
50	55	60

Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys			
65	70	75	80

Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys		
85	90	95

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val		
100	105	110

Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val		
115	120	125

Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys	
---	--

130

135

140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
1 5 10 15

Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
20 25 30

Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
35 40 45

Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
50 55 60

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
65 70 75 80

Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
85 90 95

Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
100 105 110

Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
115 120 125

Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
130 135 140

Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
 1 5 10 15
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
 20 25 30
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
 35 40 45
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
 50 55 60
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 65 70 75 80
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu
 85 90 95
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp
 100 105 110
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr
 115 120 125
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe
 130 135 140
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
 1 5 10 15
 Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
 20 25 30
 Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
 35 40 45
 Glu Glu Glu Asn Leu Glu Lys Val Glu Lys Leu Ile Pro Glu Asp
 50 55 60
 Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys
 65 70 75 80
 Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys
 85 90 95

Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
100								105						110	
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
115							120						125		
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys
130						135							140		
Trp	Lys	Asn	Lys	Gly	Arg	Pro	Gln	Leu	Tyr	Tyr	Val	Thr	Leu		
145						150					155				

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu	Val	Asp	Val	Asp	Asn	Gln	Ala	Asp	Asn	His	Gly	Ile	His	Ser	Ala
1							5			10			15		
Leu	Lys	Thr	Cys	Glu	Glu	Ile	Lys	Glu	Ala	Lys	Thr	Leu	Tyr	Ser	Trp
						20			25			30			
Ile	Gln	Lys	Val	Ile	Arg	Cys	Arg	Asn	Gln	Ser	Gln	Ser	His	Tyr	Lys
					35		40					45			
Asp	Leu	Glu	Asp	Ile	Lys	Ile	Phe	Ala	Gln	Thr	Asn	Ile	Val	Ala	Thr
					50		55				60				
Pro	Arg	Asp	Tyr	Asn	Glu	Glu	Asp	Phe	Lys	Val	Ile	Ala	Arg	Lys	Glu
					65		70			75			80		
Val	Phe	Ser	Thr	Gly	Leu	Met	Ile	Glu	Leu	Ile	Asp	Lys	Cys	Leu	Val
					85				90			95			
Glu	Leu	Leu	Ser	Ser	Ser	Asp	Val	Ser	Asp	Arg	Gln	Lys	Leu	Gln	Cys
						100			105			110			
Phe	Gly	Phe	Gln	Leu	Lys	Gly	Asn	Gln	Leu	Ala	Lys	Thr	His	Leu	Leu
						115			120			125			
Thr	Ala	Leu	Ser	Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	Asn
						130			135			140			
Gln	Val	Arg	Ala	Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	Thr
					145				150			155			160
Lys	Tyr	Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	Phe
					165				170			175			
Cys	Gly	Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	Asp
					180				185			190			

Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655
 Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln
 660 665 670
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn
 675 680 685
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys
 690 695 700
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr
 705 710 715 720
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln
 725 730 735
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu
 740 745 750
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu
 755 760 765
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu
 770 775 780
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile
 785 790 795 800
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln
 805 810 815
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp
 820 825 830
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly
 835 840 845
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu
 850 855 860

Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
 865 870 875 880
 Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
 885 890 895
 Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
 900 905 910
 Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
 915 920 925
 Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
 930 935 940
 Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
 945 950 955 960
 Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
 965 970 975
 Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe
 980 985 990
 Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTCAAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCCAGG AGTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 22..1716
(D) OTHER INFORMATION: /note= "EcoRI-NotI insert of
clone 712562 encoding 63 kDa

telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC	TGCACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGAGCTG	180
TCGGAAGCAG	AGGTCAAGGCA	GCATCGGGAA	GCCAGGCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGARGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCGG	CGCCCCGGCC	TCCTGGCGC	CTCTGTGCTG	420
GGCCTGGACG	ATATCCACAG	GGCCTGGCGC	ACCTTCGTGC	TGCGTGTGCG	GGCCCAGGAC	480
CCGCGCCTG	AGCTGTACTT	TGTCAAGGTG	GATGTGACGG	GCGCGTACGA	CACCATCCCC	540
CAGGACAGGC	TCACGGAGGT	CATGCCAGC	ATCATCAAAC	CCCAGAACAC	GTACTGCGTG	600
CGTCGGTATG	CCGTGGTCCA	GAAGGCCGCC	ATGGGCACGT	CCGCAAGGCC	TTCAAGAGCC	660
ACGT CCTACG	TCCAGTGCCA	GGGGATCCCG	CAGGGCTCCA	TCCTCTCCAC	GCTGCTCTGC	720
AGCCTGTGCT	ACGGCGACAT	GGAGAACAAAG	CTGTTGCGG	GGATTGGCG	GGACGGGCTG	780
CTCCTGCGTT	TGGTGGATGA	TTTCTTGTG	GTGACACCTC	ACCTCACCCA	CGCGAAAACC	840
TTCCCTCAGGA	CCCTGGTCCG	AGGTGTCCCT	GAGTATGGCT	GCGTGGTGAA	CTTGCGGAAG	900
ACAGTGGTGA	ACTTCCCTGT	AGAAGACGAG	GCCCTGGGTG	GCACGGCTTT	TGTTCAGATG	960
CCGGCCCCACG	GCCTATTCCC	CTGGTGGCGC	CTGCTGCTGG	ATACCCGGAC	CCTGGAGGTG	1020
CAGAGCGACT	ACTCCAGCTA	TGCCCCGACC	TCCATCAGAG	CCAGTCTCAC	CTTCAACCGC	1080
GGCTTCAAGG	CTGGGAGGAA	CATGCGTCGC	AAACTCTTG	GGGTCTTGCG	GCTGAAGTGT	1140
CACAGCCTGT	TTCTGGATTT	GCAGGTGAAC	AGCCTCCAGA	CGGTGTGCAC	CAACATCTAC	1200
AAGATCCTCC	TGCTGCAGGC	GTACAGGTTT	CACGCATGTG	TGCTGCAGCT	CCCATTTCAT	1260
CAGCAAGTTT	GGAGAACCCC	ACATTTTCC	TGCGCGTCAT	CTCTGACACG	GCTCCCTCTG	1320
CTACTCCATC	CTGAAAGCCA	AGAACGCAGG	GATGTCGCTG	GGGGCCAAGG	GCGCCGCCGG	1380
CCCTCTGCC	TCCGAGGCCG	TGCAGTGGCT	GTGCCACCAA	GCATTCTGC	TCAAGCTGAC	1440
TCGACACCGT	GTCACCTACG	TGCCACTCCT	GGGGTCACTC	AGGACAGCCC	AGACGCAGCT	1500
GAGTCGGAAG	CTCCCGGGGA	CGACGCTGAC	TGCCCTGGAG	GCCGCAGCCA	ACCCGGCACT	1560
GCCCTCAGAC	TTCAAGACCA	TCCTGGACTG	ATGGCCACCC	GCCCACAGCC	AGGCGAGAG	1620
CAGACACCAAG	CAGCCCTGTC	ACGCCGGGCT	TATACTGCCC	AGGGAGGGAG	GGGCGGCCCA	1680
CACCCAGGCC	TGCACCGCTG	GGAGTCTGAG	GCCTGAGTGA	GTGTTGGCC	GAGGCCTGCA	1740

TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA	1800
GTGTCCAGCA CACCTGCGTT TTCACTTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC	1860
CAGCTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG	1920
ATTCGCCATT GTTCACCCCTT CGCCCTGCCT TCCTTGCCCT TCCACCCCCA CCATTCAGGT	1980
GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGGAAATTGG AGTGACCAAA GGTGTGCCCT	2040
GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG	2100
TGCTGTGGGA GTAAAATACT GAATATATGA GTTTTCAGT TTTGGAAAAA AAAAAAAAAA	2160
AAAAAAAAAA A	2171

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..564
 - (D) OTHER INFORMATION: /note= "63 kDa telomerase protein encoded by ORF of EcoRI-NotI insert of clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr			
1	5	10	15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val			
20	25	30	
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val			
35	40	45	
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala			
50	55	60	
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp			
65	70	75	80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr			
85	90	95	
Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala			
100	105	110	
Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu			
115	120	125	

Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
 130 135 140
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
 145 150 155 160
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
 165 170 175
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
 180 185 190
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
 195 200 205
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 210 215 220
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 225 230 235 240
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 245 250 255
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 260 265 270
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 275 280 285
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 290 295 300
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 305 310 315 320
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460

Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
465 470 475 480

Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
485 490 495

Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
500 505 510

Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
515 520 525

Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
530 535 540

Thr Ser Gln Gly Gly Arg Gly Pro His Pro Gly Leu His Arg Trp
545 550 555 560

Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
1 5 10 15

Tyr Arg Lys Ser Val Trp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
1 5 10 15

Val Arg Gln His Arg Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
1 5 10 15

Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
1 5 10 15

Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly
1 5 10 15

Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Thr Lys Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
1 5 10 15

Tyr Tyr Ala Thr Leu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
20 25 30

Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40 45

Asp Asp Tyr Leu Leu Ile Thr
50 55

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
1 5 10 15

Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
20 25 30

Val Val

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
1 5 10 15

Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
20 25 30

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Lys Val Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTT TTTGTGTCAT TTCTATATGG 60

AAGATTTGAT TGATGAATAC CTATCGTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG 120

TAGTCGACGA CTACCTCCTC ATCACC 146

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe
1 5 10 15

Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys
 20 25 30

Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

GACGATTTC C TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Asp Phe Leu Phe Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAAAAAAAAA AAAAAAA

16

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTTTTTTTTTT TTTTTTT

17

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15

Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
20 25 30

Asp Ile Trp
35

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
1 5 10 15

Asn Leu Arg Lys Arg Phe
20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /note= "motif 3(A) peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe.
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
20 25 30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn	Glu	Phe	Arg	Ile
1				5					10					15	
Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp							
		20					25								

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile
1				5					10					15	
Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
		20					25								

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1				5				10							15
Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe
	20							25						30	

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: /note= "motif 5(C) peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser	Thr	Asp	Gln
1					5				10						15
Gln	Gln	Val	Ile	Asn	Ile	Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys
	20							25						30	
Tyr	Asn	Ala	Lys	Ala	Asn	Arg	Asp	Lys	Ile	Leu	Ala	Val	Ser	Ser	Gln
	35						40						45		
Ser															

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /note= "motif 0 peptide from Euploites aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30

Asn Ile Trp
35

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..23
 - (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15

Thr Phe Asn Lys Lys Ile Val
20

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..26
 - (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
1 5 10 15

Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15

Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu
1 5 10 15

Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu
20 25 30

Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif 1 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln
1 5 10 15

Lys Ser Tyr Ser Lys Thr
20

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "motif 0 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys
1 5 10 15

Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15

Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala
20 25

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "motif C peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile
1 5 10 15

Thr Thr Gln Glu Asn Asn
20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser
1 5 10 15

Asp Leu Arg Asn Arg Thr
20

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys
1 5 10 15
Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg
1 5 10 15
Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /note= "motif B peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile
1 5 10 15

Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
20 25

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif C peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile
1 5 10 15

Thr Val Asn Lys Lys Asp
20

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "motif D peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif 1 peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
1 5 10 15

Ser Thr Val Thr Ile Val
20

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "motif 0 peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
1 5 10 15

Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro	Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser
1					5					10					15
Ile	Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys					
			20						25						

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Glu	Asp	Lys	Cys	Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser
1						5				10					15
Leu	Ser	Ala	Pro	Ile	Val	Asp	Leu	Val	Tyr	Asp					
			20					25							

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif C peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
1 5 10 15
Ser Thr Asp Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "motif D peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif 1 peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
1 5 10 15
Phe Gln Lys Asn Arg Leu
20

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5 10 15

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /note= "motif A peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
1 5 10 15

Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
20 25

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Arg	Ala	Thr	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile
1				5						10				15	
Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly					
			20					25							

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val
1				5					10				15		
Thr	Pro	His	Leu	Thr	His										
			20												

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY:
(B) LOCATION: 1..4029
(D) OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC	60
GCGCGCTCCC CGCTGCCGAG CGGTGGCTC CCTGCTGGCG AGCCACTACC GCGAGGTGCT	120
GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAAGCGCG	180
GGACCCGGCG GCTTCCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN	240
ANGGCNGCCC CCCGCCGCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC	300
CCGAGTGCTG CANANGCTGT GCGANCACGG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC	360
GCTGCTGGAC GGGGCCCGCG GGGGCCCCCCC CGAGGCCTTC ACCACCAGCG TGCGCAGCTA	420
CCTGCCAAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGC TGCTGCTGCG	480
CCGCGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT	540

GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATA	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGCA	GGGGTCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTGGAG	GGTGCCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCA	1200
GCGNTACTGG	CAAATGCGGC	CCCTGTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGC	1260
CTACGGGGTG	TTCCCTCAAGA	CGCACTGCC	GCTGCGAGCT	GCGGTACCCC	CAGCAGCCGG	1320
TGTCTGTGCC	CGGGAGAAC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTCG	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560
CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	TTTCAAAAG	AACAGGCTCT	TTTCTACCG	GAAGAGTGT	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTCGGAAG	1860
CAGAGGTCA	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCTG	GGAGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTCAGCG	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCAGGGCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGC	ACGTCCGCAA	GGCCTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA	2400

GGCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG	2460
GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCACATC AGGGGCAAGT	2520
CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC	2580
TGTGCTACGG CGACATGGAG AACAAAGCTGT TTGCGGGGAT TCGGCAGGAC GGGCTGCTCC	2640
TGCCTTTGGT GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC	2700
TCAGGACCCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCCT GGTGAACCTG CGGAAGACAG	2760
TGGTGAACCTT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC GGCTTTGTT CAGATGCCGG	2820
CCCACGGCCT ATTCCCCTGG TGCGGCCTGC TGCTGGATAC CCGGACCCCTG GAGGTGCAGA	2880
GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT	2940
TCAAGGCTGG GAGGAACATG CGTCGAAAC TCTTGGGAT CTTGCGCTG AAGTGTACACA	3000
GCCTGTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA	3060
TCCTCCTGCT GCAGGCGTAC AGGTTTCAAG CATGTGTGCT GCAGCTCCCA TTTCATCAGC	3120
AAGTTTGGAA GAACCCACA TTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT	3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC	3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCTGCTC AAGCTGACTC	3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCAG ACGCAGCTGA	3360
GTCGGAAGCT CCCGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACACTG	3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC	3540
CCAGGCCCGC ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCCAGGGCC	3720
AGCTTTCTT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCCTGA GAAGGGACCTT GGGAGCTCTG GGAATTGGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTCAGTT TTGAAAAAAA AAAAAAAA	4020
AAAAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1 5 10 15

Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20 25 30

Ala Gln Pro Leu Pro Arg Gly Ala Ala Ala Gly His Val Arg Ala Ala
35 40 45

Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50 55 60

Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa
65 70 75 80

Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu
85 90 95

Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu
100 105 110

Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly
115 120 125

Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His
130 135 140

Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala
145 150 155 160

Pro Arg Gly Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa
165 170 175

Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala
180 185 190

Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg
195 200 205

Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala
210 215 220

Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu
225 230 235 240

Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln
245 250 255

Ala Trp Arg Cys Pro
260

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln
1 5 10 15

Asp Ala Trp Thr Glu
20

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
1 5 10 15

Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
20 25 30

Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
35 40 45

Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
50 55 60

Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
65 70 75 80

Tyr Ile

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
 1 5 10 15
 Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
 20 25 30
 Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
 35 40 45
 Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
 50 55 60
 His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
 65 70 75 80
 Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
 85 90 95
 Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
 100 105 110
 Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
 115 120 125
 Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
 130 135 140
 Ser Met Pro Ser Ser Arg Cys Arg Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
 1 5 10 15
 Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser
 20 25 30
 Cys Thr Gly
 35

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg
1 5 10 15

Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly
20 25 30

Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr
35 40

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile
1 5 10 15

Gly Lys Pro Gly Pro Pro Cys
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
1 5 10 15
Pro Ser Val Ser Pro Arg Gly
20

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1 5 10 15
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
20 25 30
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
35 40 45
Thr Leu Ser Arg Trp Met
50

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1 5 10 15
Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
20 25 30
Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
35 40 45
Thr Ser Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
1 5 10 15
Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Gly Met Pro Ser Ser Ser Arg Ala Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
20 25 30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
35 40 45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
50 55 60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp
65 70

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
20

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Thr Cys Gly Arg Gln Trp
1 5

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
50 55 60

Ser Leu Gly Ser Cys Gly
65 70

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
1 5 10 15

Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser
20 25 30

Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg
35 40 45

Pro Pro Ser Ala Thr Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
1 5 10 15

Pro Arg Arg Ser
20

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Val Gly Ser Ser Arg Gly Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
1 5 10 15

Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Leu Ser Glu Cys Pro Ala Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg
1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu
20 25 30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
20 25 30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
35 40 45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50 55 60

Ala Val Gly Val Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
 20 25 30

Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
 35 40 45

Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
 50 55 60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
 65 70 75 80

Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
 85 90 95

Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
 100 105 110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 115 120 125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 130 135 140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 145 150 155 160

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
 165 170 175

Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
 180 185 190

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 195 200 205

Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
 1 5 10 15

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 20 25 30

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
 50 55 60
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 65 70 75 80
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 85 90 95
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
 100 105 110
 Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
 115 120 125
 Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
 130 135 140
 Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
 145 150 155 160
 Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
 165 170 175
 Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
 180 185 190
 His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
 195 200 205
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
 210 215 220
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu His Arg Pro Pro Ser
 225 230 235 240
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
 245 250 255
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
 260 265 270
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg
1 5 10 15

Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys
20 25 30

Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys
35 40 45

His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Gly Ala Val
50 55 60

Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp
65 70 75 80

Val Gln Thr Pro Leu His Pro Gln Ala
85

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn
1 5 10 15

Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly
20 25 30

Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro
35 40 45

Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His
50 55 60

Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15

Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 30

His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45

Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60

Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80

Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60

Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
1 5 10 15

Asp Pro Gly Pro Arg Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
1 5 10 15

Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
20 25 30

Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
35 40 45

Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
50 55 60

Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
65 70 75 80

Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
85 90 95

Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
100 105 110

Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile
115 120 125

Ser Ser Ala Ser Leu Glu Pro His Ile Phe Pro Ala Arg His Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Gly Leu Pro Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp

1	5	10	15												
Val	Ala	Gly	Gly												
		Gln	Gly												
		Arg	Arg												
		Arg	Pro												
		Ser	Ala												
		Leu	Arg												
			Gly												
			Arg												
		20	25	30											
Ala	Val	Ala	Val	Pro	Pro	Ser	Ile	Pro	Ala	Gln	Ala	Asp	Ser	Thr	Pro
							35						40		45
Cys	His	Leu	Arg	Ala	Thr	Pro	Gly	Val	Thr	Gln	Asp	Ser	Pro	Asp	Ala
							50						55		60
Ala	Glu	Ser	Glu	Ala	Pro	Gly	Asp	Asp	Ala	Asp	Cys	Pro	Gly	Gly	Arg
							65						75		80
Ser	Gln	Pro	Gly	Thr	Ala	Leu	Arg	Leu	Gln	Asp	His	Pro	Gly	Leu	Met
							85						90		95
Ala	Thr	Arg	Pro	Gln	Pro	Gly	Arg	Glu	Gln	Thr	Pro	Ala	Ala	Leu	Ser
							100						105		110
Arg	Arg	Ala	Leu	Arg	Pro	Arg	Glu	Gly	Gly	Ala	Ala	His	Thr	Gln	Ala
							115						120		125
Arg	Thr	Ala	Gly	Ser	Leu	Arg	Pro	Glu							
							130						135		

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Val	Phe	Gly	Arg	Gly	Leu	His	Val	Arg	Leu	Lys	Ala	Glu	Cys	Pro	Ala
1					5									10	15
Glu Ala															

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala	Ser	Val	Gln	Pro	Arg	Ala	Glu	Cys	Pro	Ala	His	Leu	Pro	Ser	Ser
1							5						10		15

Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro
20 25 30

His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro
35 40 45

Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro
50 55 60

Pro Pro Ser Arg Trp Arg Pro
65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro
1 5 10 15

Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser
20 25 30

Asn Trp Gly Glu Val Leu Trp Glu
35 40

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys
1 5 10 15

Lys Lys

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro
1 5 10 15

Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys
20 25 30

Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala
35 40 45

Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu
50 55 60

Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa
65 70 75 80

Gly Xaa Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala
85 90

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg
1 5 10 15

Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly
20 25 30

Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr
35 40 45

Arg

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
 1 5 10 15
 Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
 20 25 30
 Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
 35 40 45
 Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
 50 55 60
 Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
 65 70 75 80
 Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
 85 90 95
 Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
 100 105 110
 Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
 115 120 125
 Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
 130 135 140
 Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
 145 150 155 160
 Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175
 Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190
 Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Arg Arg
 195 200 205
 Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220
 Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335

Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670

Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 805 810 815
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 820 825 830
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 835 840 845
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 850 855 860
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
1 5 10 15
His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
20 25 30
Pro Ala Pro Leu Gly Val
35

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
1 5 10 15
Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
20 25 30
Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
85 90

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Val Phe Gln Phe
1

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4015 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: cDNA
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 56..3454
 - (D) OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC							106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
5	10				15		
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC							154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro							
20	25			30			
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG							202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala							
35	40			45			
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC							250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro							
50	55		60			65	
CCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG							298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val							
70	75			80			
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG							346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu							
85	90			95			
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG							394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu							
100	105			110			
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC							442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp							
115	120			125			

GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC 490
 Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
 130 135 140 145
 GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG 538
 Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
 150 155 160
 GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG 586
 Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
 165 170 175
 CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC 634
 Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
 180 185 190
 CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG 682
 Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
 195 200 205
 GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG 730
 Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
 210 215 220 225
 GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC 778
 Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
 230 235 240
 GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC 826
 Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
 245 250 255
 CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG 874
 His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
 260 265 270
 TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC 922
 Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
 275 280 285
 TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG 970
 Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
 290 295 300 305
 GGC CCC CCA TCC ACA TCG CGG CCA CGT CCC TGG GAC ACG CCT TGT 1018
 Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys
 310 315 320
 CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC 1066
 Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
 325 330 335
 AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC 1114
 Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser
 340 345 350
 CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG 1162
 Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg
 355 360 365
 CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC 1210
 Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg

370	375	380	385	
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390	395	400		1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405	410	415		1306
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420	425	430		1354
TCT GTG GCG GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435	440	445		1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450	455	460	465	
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470	475	480		1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485	490	495		1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500	505	510		1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515	520	525		1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530	535	540	545	
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550	555	560		1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565	570	575		1786
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580	585	590		1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595	600	605		1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610	615	620	625	

AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GCG CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys	2698

870	875	880	
ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val	885	890	2746
GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTC GAA GAC GAG GCC Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala	900	905	2794
CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro	915	920	2842
TGG TGC GGC CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp	930	935	2890
TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn	950	955	2938
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val	965	970	2986
TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser	980	985	3034
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala	995	1000	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val	1010	1015	3130
1020	1025		
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser	1030	1035	3178
1040			
CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly	1045	1050	3226
1055			
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu	1060	1065	3274
1070			
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr	1075	1080	3322
1085			
GTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg	1090	1095	3370
1100	1105		
AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro	1110	1115	3418
1120			

GCATCTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCCACAG	3471
Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp	
1125	1130
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTGGC	3591
CGAGGCCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCCTCGGC	3711
TCCACCCCCAG GGCCAGCTTT TCCTCACCAAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTGCC ATTGTTCAAC CCTCGCCCTG CCCTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTC AGTTTGAAA	4011
AAAA	4015

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser	
1 5 10 15	
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	
20 25 30	
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	
35 40 45	
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	
50 55 60	
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu	
65 70 75 80	
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val	
85 90 95	
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro	
100 105 110	
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr	
115 120 125	
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val	
130 135 140	

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130